GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:34:06 ; Search time 265.48 Seconds
(without alignments)
782.532 Million cell updates/sec

Title: US-09-719-017A-1
Perfect score: 121
Sequence: 1 gaattccctgttgacaatta.....tatctaaggaaatacttaca 121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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10: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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17: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	121	100.0	121	21	AAZ45324	Nucleotide sequenc
2	121	100.0	1793	21	AAA47190	Nucleotide sequenc
3	121	100.0	1793	21	AAZ45325	Nucleotide sequenc
4	59.2	48.9	695	12	AAQ11856	Sequence of plasmi
5	54.8	45.3	59	15	AAQ53901	Trp promoter used
6	54.8	45.3	60	21	AAA12878	Trp promoter, SEQ
7	50	41.3	59	15	AAQ53902	Lamda CII ribosome
8	50	41.3	59	21	AAA12877	Bacteriophage lamb
9	44	36.4	77	16	AAT00582	TRP promotor. Esc
10	44	36.4	77	18	AAT73712	Tryptophan promote
11	43.6	36.0	357	21	AAC64251	Trp promoter used
12	43.6	36.0	357	21	AAA95073	trp promoter. Uni
13	43.2	35.7	1519	20	AAV81508	High expression tr
14	43.2	35.7	1519	21	AAA73025	Transglutaminase n
15	42.8	35.4	63	6	AAN50137	Trp promoter. AA
16	42.2	34.9	305	14	AAQ49722	Trp promoter EcoRI
17	42	34.7	47	9	AAN80245	Sequence of synthe
18	42	34.7	74	13	AAQ31933	Trp-promoter [M1 (
19	42	34.7	86	3	AAN20110	Trp promoter. Syn
20	42	34.7	102	11	AAQ03558	EcoRI-PstI fragmen
21	42	34.7	103	6	AAN50704	Synthetic DNA sequ
22	42	34.7	103	8	AAN70717	Sequence of a synt
23	42	34.7	103	9	AAN80723	Human SP5 #19. Ho
24	42	34.7	103	10	AAN93089	Synthetic tryptoph
25	42	34.7	105	9	AAN81566	Trp promoter III g
26	42	34.7	107	6	AAN50168	Synthetic promoter
27	42	34.7	107	7	AAN60090	Sequence of synthe
28	42	34.7	107	8	AAN70163	Sequence of synthe
29	42	34.7	107	8	AAN70602	trp promoter used
30	42	34.7	107	12	AAQ13118	Synthetic trp prom
31	42	34.7	107	16	AAQ79932	trp promoter seque
32	42	34.7	111	7	AAN60088	Sequence of synthe
33	42	34.7	111	12	AAQ13116	Synthetic trp prom
34	42	34.7	137	8	AAN70250	Sequence of trp pr
35	42	34.7	141	3	AAN20014	Plasmid fragment.
36	42	34.7	151	22	AAC69044	Modified trp promo
37	42	34.7	166	10	AAN91224	Components of E. c
38	42	34.7	167	7	AAN60089	Sequence of synthe
39	42	34.7	167	12	AAQ13117	Synthetic trp prom
40	42	34.7	167	12	AAQ14900	EcoRI-ClaI fragmen
41	42	34.7	168	13	AAQ28382	E. coli trp promot
42	42	34.7	172	12	AAQ13327	EcoRI-ClaI fragmen
43	42	34.7	172	14	AAQ36948	pAT153 partial seq
44	42	34.7	172	15	AAQ66387	V-min gene detecti
45	42	34.7	264	13	AAQ25936	PDGF A chain expre

ALIGNMENTS

RESULT 1
AAZ45324
ID AAZ45324 standard; DNA; 121 BP.
XX
AC AAZ45324;
XX
DT 27-MAR-2000 (first entry)
XX
DE Nucleotide sequence of the Ptrp promoter.
XX
KW Tryptophan promoter; Ptrp promoter; heterologous protein expression;
KW Escherichia coli W; industrial protein production; enzyme; nitrilase; ss.
XX
OS Unidentified.
XX
PN WO9964607-A1.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-FR01343.
XX
PR 10-JUN-1998; 98FR-0007474.
XX
PA (RHON) RHONE-POULENC NUTRITION ANIMALE.
XX
PI Pierrard J, Guitton C, Favre-Bulle O;
XX
DR WPI; 2000-097541/08.
XX
PT Industrial production of heterologous proteins in Escherichia coli
PT strain W, particularly for expressing enzymes -
XX

```
PS   Claim 15; Page 36; 52pp; French.
XX
CC   The present sequence represents the tryptophan promoter (Ptrp promoter).
CC   The promoter was extracted from plasmid pRPA6BCAT6 by restriction digest.
CC   The promoter is used to control the expression of a heterologous
CC   protein in an expression cassette which is used to modify a strain of
CC   Escherichia coli W. The modified strain is then used for industrial
CC   production of heterologous proteins. Specifically, the promoter was
CC   used to control the expression of an Alcaligenes nitrilase gene.
CC   The method is especially used to produce proteins of relatively
CC   low value, preferably enzymes and specifically nitrilases.
XX
SQ   Sequence 121 BP; 37 A; 27 C; 23 G; 34 T; 0 other;


  Query Match             100.0%;  Score 121;  DB 21;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-29;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 gaattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcagg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gaattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcagg 60

Qy      61 tcgacctgcagccaagcttgggcatacattcaatcaattgttatctaaggaaatacttac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 tcgacctgcagccaagcttgggcatacattcaatcaattgttatctaaggaaatacttac 120

Qy     121 a 121
           |
Db     121 a 121


RESULT   2
AAA47190
ID   AAA47190 standard; DNA; 1793 BP.
XX
AC   AAA47190;
XX
DT   03-OCT-2000  (first entry)
XX
DE   Nucleotide sequence of the expression cassette of pRPA-BCAT41.
XX
KW   Methionine; 2-hydroxy-4-methylthiobutanoic acid; nitrilase;
KW   nitrile hydratase; amidase; pRPA-BCAT41; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             123..1193
FT                   /*tag= a
XX
PN   WO200036120-A1.
XX
PD   22-JUN-2000.
XX
PF   10-DEC-1999;   99WO-FR03089.
XX
PR   11-DEC-1998;   98FR-0015849.
PR   19-JUL-1999;   99FR-0009489.
XX
PA   (RHON ) RHONE-POULENC ANIMAL NUTRITION SA.
XX
PI   Favre-Bulle O,  Pierrard J,  Batisse Debitte N;
XX
DR   WPI; 2000-431598/37.
DR   P-PSDB; AAY93908.
XX
PT   Selecting sequences encoding enzymes involved in methionine synthesis,
PT   useful for hydrolysis of nitrile groups, by transforming methionine
PT   auxotrophs and selection for growth -
XX
PS   Example 1; Page 27-29; 38pp; French.
XX
CC   The specification describes a process for the selection and/or isolation
CC   of DNA sequences that encode enzymes involved in bioconversion of
CC   substrates to methionine or its derivatives such as
CC   2-hydroxy-4-methylthiobutanoic acid. DNA fragments are cloned into
CC   a microbial expression vector and recombinant vectors used to transform
CC   a host that is auxotrophic for methionine (Met). The cells are cultured
CC   in medium containing an adequate amount of substrate and microbes able
CC   to grow on this medium are selected and/or isolated. DNA sequences
CC   involved in conversion of substrates are then isolated and/or identified.
CC   The method is used to identify DNA sequences encoding nitrilases, nitrile
CC   hydratases or amidases. Nitrilases are useful in many synthetic process
CC   that require hydrolysis of nitrile groups, e.g. for production of the
CC   hydroxy analogue of Met. The present sequence is the nucleotide sequence
CC   of the expression cassette of pRPA-BCAT41.
XX
SQ   Sequence 1793 BP; 412 A; 527 C; 478 G; 376 T; 0 other;


  Query Match             100.0%;  Score 121;  DB 21;  Length 1793;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-29;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 gaattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcagg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gaattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcagg 60

Qy      61 tcgacctgcagccaagcttgggcatacattcaatcaattgttatctaaggaaatacttac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 tcgacctgcagccaagcttgggcatacattcaatcaattgttatctaaggaaatacttac 120

Qy     121 a 121
           |
Db     121 a 121


RESULT   3
AAZ45325
ID   AAZ45325 standard; DNA; 1793 BP.
XX
AC   AAZ45325;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Nucleotide sequence of an expression cassette encoding a nitrilase.
XX
KW   Tryptophan promoter; Ptrp promoter; heterologous protein expression;
KW   Escherichia coli W; industrial protein production; enzyme; nitrilase; ss.
XX
OS   Synthetic.
OS   Alcaligenes faecalis.
XX
FH   Key             Location/Qualifiers
FT   CDS             123..1193
FT                   /*tag= a
FT                   /product= "nitrilase"
XX
PN   WO9964607-A1.
XX
PD   16-DEC-1999.
XX
PF   08-JUN-1999;   99WO-FR01343.
XX
PR   10-JUN-1998;   98FR-0007474.
XX
PA   (RHON ) RHONE-POULENC NUTRITION ANIMALE.
XX
PI   Pierrard J,  Guitton C,  Favre-Bulle O;
XX
DR   WPI; 2000-097541/08.
DR   P-PSDB; AAY54121.
XX
PT   Industrial production of heterologous proteins in Escherichia coli
PT   strain W, particularly for expressing enzymes -
```

```
XX
PS   Example 1; Page 36-38; 52pp; French.
XX
CC   The present sequence represents an expression cassette comprising
CC   the tryptophan promoter (Ptrp promoter) and DNA encoding an Alcaligenes
CC   faecalis ATCC8750 nitrilase (nitB). The nitrilase polynucleotide and the
CC   promoter sequence were extracted from plasmid pRPA6BCAT6 by restriction
CC   digest. The Ptrp promoter is used to control the expression of a
CC   heterologous protein in an expression cassette which is used to modify
CC   a strain of Escherichia coli W. The modified strain is then used for
CC   industrial production of heterologous proteins. Specifically, the
CC   promoter is used to control the expression of an Alcaligenes nitrilase
CC   gene. The method is especially used to produce proteins of relatively
CC   low value, preferably enzymes and specifically nitrilases.
XX
SQ   Sequence 1793 BP; 412 A; 527 C; 478 G; 376 T; 0 other;


  Query Match             100.0%;  Score 121;  DB 21;  Length 1793;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-29;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gaattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcagg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gaattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcagg 60

Qy     61 tcgacctgcagccaagcttgggcatacattcaatcaattgttatctaaggaaatacttac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 tcgacctgcagccaagcttgggcatacattcaatcaattgttatctaaggaaatacttac 120

Qy    121 a 121
          |
Db    121 a 121


RESULT   4
AAQ11856
ID   AAQ11856 standard; DNA; 695 BP.
XX
AC   AAQ11856;
XX
DT   31-JUL-1991  (first entry)
XX
DE   Sequence of plasmid pHbCAT encoding VHb structural haemoglobin gene.
XX
KW   Haemoglobin; fermentation; brewing; ds.
XX
OS   Vitreoscilla sp.
XX
FH   Key             Location/Qualifiers
FT   misc_signal     1..91
FT                   /*tag=  a
FT                   /label= trp promoter and synthetic RBS
FT   mat_peptide     92..529
FT                   /*tag=  b
FT                   /label= Vitreoscilla structural gene
XX
PN   WO9106641-A.
XX
PD   16-MAY-1991.
XX
PF   26-OCT-1990;   90WO-US06083.
XX
PR   30-OCT-1989;   89US-0429093.
XX
PA   (CALY ) CALIF INST OF TECHN.
XX
PI   Bailey JE,  Khosla CS;
XX
DR   WPI; 1991-164191/22.
XX
PT   Enhancing cell growth - preparing foreign proteins, by
PT   co-expressing haemoglobin gene.
XX
PS   Disclosure; Page 47; 84pp; English.
XX
CC   By coexpressing a desired DNA sequence in a plasmid with the
CC   haemoglobin structural gene, expression may be regulated by the
CC   level of disolved oxygen, presence of cAMP-CAP and/or a complex
CC   nitrogen source. The method is especially useful in the production
CC   of haemoglobins and metabolites, fermentation, brewing, enzymatic
CC   degradation, waste treatment etc.
XX
SQ   Sequence 695 BP; 184 A; 147 C; 176 G; 186 T; 2 other;


  Query Match             48.9%;  Score 59.2;  DB 12;  Length 695;
  Best Local Similarity   95.3%;  Pred. No. 2.5e-09;
  Matches   61;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 aattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcaggt 61
          | | ||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      3 attcccctgttgacaattaatcatccaactagttaactagtacgcagcttggctgcaggt 62

Qy     62 cgac 65
          ||||
Db     63 cgac 66


RESULT   5
AAQ53901
ID   AAQ53901 standard; DNA; 59 BP.
XX
AC   AAQ53901;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Trp promoter used in expression vector.
XX
KW   Saporin; restenosis; melanoma; carcinoma; ovarian cancer;
KW   cytotoxin; fusion protein; targetting; internalisation; ligand;
KW   receptor; cell surface; ss.
XX
OS   Synthetic.
XX
PN   WO9325688-A.
XX
PD   23-DEC-1993.
XX
PF   14-JUN-1993;   93WO-US05702.
XX
PR   16-JUN-1992;   92US-0901718.
XX
PA   (PRIZ-) PRIZM PHARM INC.
PA   (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
XX
PI   Baird JA,  Barthelemy I,  Lappi DA,  Sosnowski BA;
XX
DR   WPI; 1994-007545/01.
XX
PT   Recombinant fusion proteins contg. saporin - having an N-terminal
PT   extension to permit recombinant expression and opt. to target the
PT   protein to target cells
XX
PS   Example 2; Page 33; 62pp; English.
XX
CC   Recombinant fusion proteins containing saporin can be used for
CC   treating diseases such as restenosis, human melanomas and human
CC   ovarian carcinomas.  The proteins comprise saporin with an N-
CC   terminal extension, the saporin containing protein being cytotoxic
CC   upon internalisation by a eukaryotic cell.  The N-terminal extension
CC   may include a ligand e.g. basic fibroblast growth factor (bFGF),
CC   that specifically interacts with a cell surface protein, thus
CC   specific cells can be targetted.  The N-terminal extension renders
CC   the resulting saporin containing protein sufficiently non-cytotoxic
CC   to allow recombinant expression.  The Trp promoter was used in
```

```
CC   constructs to regulate expression of saporin/bFGF fusion proteins.
XX
SQ   Sequence 59 BP; 17 A; 14 C; 11 G; 17 T; 0 other;


  Query Match             45.3%;  Score 54.8;  DB 15;  Length 59;
  Best Local Similarity   96.6%;  Pred. No. 3.6e-08;
  Matches   56;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 aattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcag 59
          | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 attcccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcag 59


RESULT   6
AAA12878
ID   AAA12878 standard; DNA; 60 BP.
XX
AC   AAA12878;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Trp promoter, SEQ ID NO:62.
XX
KW   Targetted gene delivery; fibroblast growth factor receptor;
KW   FGFR-binding protein; nucleic acid binding protein;
KW   receptor-internalised ligand; cytotoxin; saporin; gene therapy;
KW   cytocide; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW   rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;
KW   eczema; promoter; alpha-actin; alpha-crystallin; ribosome binding site;
KW   ss.
XX
OS   Unidentified.
XX
PN   US6037329-A.
XX
PD   14-MAR-2000.
XX
PF   24-SEP-1996;   96US-0718904.
XX
PR   15-MAR-1994;   94US-0213446.
PR   15-MAR-1994;   94US-0213447.
PR   29-AUG-1994;   94US-0297961.
PR   13-SEP-1994;   94US-0305771.
PR   16-MAY-1995;   95US-0441979.
XX
PA   (SELE-) SELECTIVE GENETICS INC.
XX
PI   Chandler LA,  Sosnowski BA,  Baird JA;
XX
DR   WPI; 2000-292008/25.
XX
PT   Gene delivery system, useful for treating or preventing cancer and
PT   rheumatoid arthritis, comprises receptor-internalized ligand linked to
PT   nucleic acid binding domain and nucleic acid  -
XX
PS   Example 6; Column 145; 131pp; English.
XX
CC   The invention relates to a novel gene delivery composition for the
CC   targetted delivery of cytotoxins or prodrug-converting enzymes to
CC   proliferating cells. The gene delivery composition comprises a protein
CC   that binds the fibroblast growth factor receptor (FGFR) which is fused
CC   or chemically conjugated to a nucleic acid binding domain. The nucleic
CC   acid binding domain is complexed with a suitable expression construct
CC   encoding a cytotoxin such as saporin. One or more linkers may join the
CC   FGFR-binding protein to the nucleic acid binding protein. These are
CC   selected to increase the specificity, toxicity, solubility, serum
CC   stability or intracellular availability, and may serve to promote
CC   condensation of nucleic acids for delivery to a cell. The fusion protein
CC   binds to FGFR and is internalised by cells that carry this receptor. The
CC   gene delivery composition is used for the therapeutic alteration of the
CC   function, gene expression and viability of cells. In particular, it may
CC   be used for the treatment and prevention of cell proliferative
CC   disorders, for example after eye surgery, melanoma and many other sorts
CC   of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC   diabetic retinopathy, psoriasis and eczema. The gene delivery
CC   compositions of the invention have high specificity for particular cells
CC   and can deliver larger amounts of DNA compared to prior art methods.
CC   Sequence AAA12925 represents the human alpha-actin promoter, and
CC   sequences AAA12923-A12924 represent PCR primers used to amplify this
CC   promoter. Sequence AAA12934 represents the human alpha-crystallin
CC   promoter, which was generated using PCR primers AAA12926-A12933. Sequence
CC   AAA12878 represents a Trp gene promoter, and sequence AAA12877 represents
CC   the cII ribosome binding site of bacteriophage lambda. All these elements
CC   may be incorporated into the cytotoxin-encoding DNA construct to be
CC   delivered to the cell. Sequence AAA12876 represents an oligonucleotide of
CC   undefined function.
XX
SQ   Sequence 60 BP; 17 A; 14 C; 12 G; 17 T; 0 other;


  Query Match             45.3%;  Score 54.8;  DB 21;  Length 60;
  Best Local Similarity   96.6%;  Pred. No. 3.7e-08;
  Matches   56;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 aattccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcag 59
          | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 attcccctgttgacaattaatcatcgaactagttaactagtacgcagcttggctgcag 60


RESULT   7
AAQ53902
ID   AAQ53902 standard; DNA; 59 BP.
XX
AC   AAQ53902;
XX
DT   22-JUN-1994  (first entry)
XX
DE   Lamda CII ribosome binding site used in expression vector.
XX
KW   Saporin; restenosis; melanoma; carcinoma; ovarian cancer;
KW   cytotoxin; fusion protein; targetting; internalisation; ligand;
KW   receptor; cell surface; ss.
XX
OS   Lambda phage.
XX
PN   WO9325688-A.
XX
PD   23-DEC-1993.
XX
PF   14-JUN-1993;   93WO-US05702.
XX
PR   16-JUN-1992;   92US-0901718.
XX
PA   (PRIZ-) PRIZM PHARM INC.
PA   (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
XX
PI   Baird JA,  Barthelemy I,  Lappi DA,  Sosnowski BA;
XX
DR   WPI; 1994-007545/01.
XX
PT   Recombinant fusion proteins contg. saporin - having an N-terminal
PT   extension to permit recombinant expression and opt. to target the
PT   protein to target cells
XX
PS   Example 2; Page 33; 62pp; English.
XX
CC   Recombinant fusion proteins containing saporin can be used for
CC   treating diseases such as restenosis, human melanomas and human
CC   ovarian carcinomas.  The proteins comprise saporin with an N-
CC   terminal extension, the saporin containing protein being cytotoxic
CC   upon internalisation by a eukaryotic cell.  The N-terminal extension
CC   may include a ligand e.g. basic fibroblast growth factor (bFGF),
CC   that specifically interacts with a cell surface protein, thus
CC   specific cells can be targetted.  The N-terminal extension renders
CC   the resulting saporin containing protein sufficiently non-cytotoxic
```

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CC   to allow recombinant expression.  The lamda CII ribosome binding
CC   site was used in constructs for expressing saporin/bFGF fusion
CC   proteins.
XX
SQ   Sequence 59 BP; 20 A; 11 C; 10 G; 18 T; 0 other;


  Query Match             41.3%;  Score 50;  DB 15;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-06;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      72 ccaagcttgggcatacattcaatcaattgttatctaaggaaatacttaca 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6 ccaagcttgggcatacattcaatcaattgttatctaaggaaatacttaca 55


RESULT   8
AAA12877
ID   AAA12877 standard; DNA; 59 BP.
XX
AC   AAA12877;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Bacteriophage lambda cII ribosome binding site, SEQ ID NO:61.
XX
KW   Targetted gene delivery; fibroblast growth factor receptor;
KW   FGFR-binding protein; nucleic acid binding protein;
KW   receptor-internalised ligand; cytotoxin; saporin; gene therapy;
KW   cytocide; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW   rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;
KW   eczema; promoter; alpha-actin; alpha-crystallin; ribosome binding site;
KW   ss.
XX
OS   Bacteriophage lambda.
XX
PN   US6037329-A.
XX
PD   14-MAR-2000.
XX
PF   24-SEP-1996;   96US-0718904.
XX
PR   15-MAR-1994;   94US-0213446.
PR   15-MAR-1994;   94US-0213447.
PR   29-AUG-1994;   94US-0297961.
PR   13-SEP-1994;   94US-0305771.
PR   16-MAY-1995;   95US-0441979.
XX
PA   (SELE-) SELECTIVE GENETICS INC.
XX
PI   Chandler LA,  Sosnowski BA,  Baird JA;
XX
DR   WPI; 2000-292008/25.
XX
PT   Gene delivery system, useful for treating or preventing cancer and
PT   rheumatoid arthritis, comprises receptor-internalized ligand linked to
PT   nucleic acid binding domain and nucleic acid  -
XX
PS   Example 6; Column 65-66; 131pp; English.
XX
CC   The invention relates to a novel gene delivery composition for the
CC   targetted delivery of cytotoxins or prodrug-converting enzymes to
CC   proliferating cells. The gene delivery composition comprises a protein
CC   that binds the fibroblast growth factor receptor (FGFR) which is fused
CC   or chemically conjugated to a nucleic acid binding domain. The nucleic
CC   acid binding domain is complexed with a suitable expression construct
CC   encoding a cytotoxin such as saporin. One or more linkers may join the
CC   FGFR-binding protein to the nucleic acid binding protein. These are
CC   selected to increase the specificity, toxicity, solubility, serum
CC   stability or intracellular availability, and may serve to promote
CC   condensation of nucleic acids for delivery to a cell. The fusion protein
CC   binds to FGFR and is internalised by cells that carry this receptor. The
CC   gene delivery composition is used for the therapeutic alteration of the
CC   function, gene expression and viability of cells. In particular, it may
CC   be used for the treatment and prevention of cell proliferative
CC   disorders, for example after eye surgery, melanoma and many other sorts
CC   of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC   diabetic retinopathy, psoriasis and eczema. The gene delivery
CC   compositions of the invention have high specificity for particular cells
CC   and can deliver larger amounts of DNA compared to prior art methods.
CC   Sequence AAA12925 represents the human alpha-actin promoter, and
CC   sequences AAA12923-A12924 represent PCR primers used to amplify this
CC   promoter. Sequence AAA12934 represents the human alpha-crystallin
CC   promoter, which was generated using PCR primers AAA12926-A12933. Sequence
CC   AAA12878 represents a Trp gene promoter, and sequence AAA12877 represents
CC   the cII ribosome binding site of bacteriophage lambda. All these elements
CC   may be incorporated into the cytotoxin-encoding DNA construct to be
CC   delivered to the cell. Sequence AAA12876 represents an oligonucleotide of
CC   undefined function.
XX
SQ   Sequence 59 BP; 20 A; 11 C; 10 G; 18 T; 0 other;


  Query Match             41.3%;  Score 50;  DB 21;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-06;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      72 ccaagcttgggcatacattcaatcaattgttatctaaggaaatacttaca 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6 ccaagcttgggcatacattcaatcaattgttatctaaggaaatacttaca 55


RESULT   9
AAT00582
ID   AAT00582 standard; DNA; 77 BP.
XX
AC   AAT00582;
XX
DT   28-MAY-1996  (first entry)
XX
DE   TRP promotor.
XX
KW   TRP; anti-phosphoglycerate mutase; PGAM; antibody; IgG; isoenzyme; ds.
XX
OS   Escherichia coli.
XX
PN   JP07258299-A.
XX
PD   09-OCT-1995.
XX
PF   25-MAR-1994;   94JP-0079867.
XX
PR   25-MAR-1994;   94JP-0079867.
XX
PA   (ORIY ) ORIENTAL YEAST CO LTD.
XX
DR   WPI; 1995-380078/49.
XX
PT   Anti-phospho:glycerate mutase isozyme specific IgG antibodies - used
PT   to detect and distinguish between M and B type isozyme(s)
XX
PS   Disclosure; Fig 2; 12pp; Japanese.
XX
CC   This sequence represents the TRP promotor.  This sequence was used in an
CC   expression vector to express anti-phosphoglycerate mutase (PGAM) M and B
CC   type isozyme specific IgG antibodies.  These antibodies were termed MM
CC   and BB respectively.  The antibodies MM and BB can be used to detect and
CC   distinguish between the two PGAM isozymes.  They can also be used in
CC   various diagnostic agents.
XX
SQ   Sequence 77 BP; 26 A; 16 C; 15 G; 20 T; 0 other;


  Query Match             36.4%;  Score 44;  DB 16;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      4 ttccctgttgacaattaatcatcgaactagttaactagtacgca 47
          ||||||||||||||||||||||||||||||||||||||||||||
Db      4 ttccctgttgacaattaatcatcgaactagttaactagtacgca 47
```

RESULT 10
AAT73712
ID AAT73712 standard; DNA; 77 BP.
XX
AC AAT73712;
XX
DT 03-MAR-1998 (first entry)
XX
DE Tryptophan promoter from Escherichia coli.
XX
KW Bisphosphoglycerate mutase; BPGM; diagnosis; haemolytic disorder;
KW immunoassay; kit; 2,3-bisphosphoglycerate; haemaglobin; anaemia; PCR;
KW primer; tryptophan promoter; ss.
XX
OS Escherichia coli.
XX
PN EP785217-A1.
XX
PD 23-JUL-1997.
XX
PF 17-JAN-1997; 97EP-0400098.
XX
PR 04-DEC-1996; 96JP-0337723.
PR 19-JAN-1996; 96JP-0024897.
XX
PA (ORIY) ORIENTAL YEAST CO LTD.
XX
PI Fujita T, Kasuya K, Matuo Y, Mori K, Tanigushi Y;
PI Uchida K;
XX
DR WPI; 1997-365901/34.
XX
PT Antibody to bis:phospho:glycerate mutase - useful in immunoassays
PT for diagnosis of haemolytic disorders
XX
PS Example 1; Figure 8; 36pp; English.
XX
CC This sequence is the tryptophan promoter which was used to direct
CC expression of human bisphophoglycerate mutase (BPGM). Recombinant
CC human BPGM was used as an antigen to prepare a novel antibody to
CC BPCM. The antibody can be used in immunoassays for BPGM. BPGM, an isozyme
CC of mammalian phosphoglycerate mutase (PGAM), catalyses synthesis and
CC decomposition of 2,3-bisphosphoglycerate (2,3-BPG), important in
CC regulating the oxygen affinity of haemoglobin in red blood cells of
CC humans and many other mammals. 2,3-BPG lowers the oxygen affinity of
CC haemoglobin, thereby promoting oxygen supply to tissues, by binding
CC directly to haemoglobin and by lowering red blood cell pH. 2,3-BPG levels
CC are abnormal in several diseases, e.g. increased in haemolytic anaemia
CC and iron deficient anaemia and decreased in diabetic ketoacidosis and
CC hexokinase deficiency. An immunoassay for BPGM in red blood cells or
CC plasma provides a marker aiding disease diagnosis e.g. of haemolytic
CC disorders. The antibody has high specificity to human BPGM, allowing
CC accurate determination of BPGM.
XX
SQ Sequence 77 BP; 26 A; 16 C; 15 G; 20 T; 0 other;

```
  Query Match             36.4%;  Score 44;  DB 18;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ttccctgttgacaattaatcatcgaactagttaactagtacgca 47
          ||||||||||||||||||||||||||||||||||||||||||||
Db      4 ttccctgttgacaattaatcatcgaactagttaactagtacgca 47
```

RESULT 11
AAC64251
ID AAC64251 standard; DNA; 357 BP.
XX
AC AAC64251;
XX
DT 23-FEB-2001 (first entry)
XX
DE Trp promoter used in a soybean cotyledon LAP expression construct.
XX
KW Trp promoter; soybean cotyledon leucine aminopeptidase; LAP;
KW Glycine max; recombinant expression; plasmid construction; ds.
XX
OS Unidentified.
XX
PN JP2000262286-A.
XX
PD 26-SEP-2000.
XX
PF 15-MAR-1999; 99JP-0068353.
XX
PR 15-MAR-1999; 99JP-0068353.
XX
PA (AJIN) AJINOMOTO KK.
XX
DR WPI; 2000-682117/67.
XX
PT Novel DNA encoding leucine aminopeptidase useful for the recombinant
PT preparation of leucine aminopeptidase -
XX
PS Example 2; Page 18-19; 22pp; Japanese.
XX
CC The invention relates to a soybean leucine aminopeptidase (AAB29636),
CC and cDNA encoding it (AAC64250), derived from cotyledon tissue. The
CC invention also relates to variants of soybean cotyledon LAP which retain
CC activity, recombinant vectors and host cells comprising DNA encoding the
CC soybean cotyledon LAP, and a method fro the recombinant production of the
CC LAP. The method of the invention can be used for the large scale
CC recombinant preparation of soybean cotyledon leucine aminopeptidase. The
CC present sequence represents a trp promoter used in a soybean cotyledon
CC leucine aminopeptidase bacterial expression construct in an
CC exemplification of the invention.
XX
SQ Sequence 357 BP; 95 A; 90 C; 82 G; 90 T; 0 other;

```
  Query Match             36.0%;  Score 43.6;  DB 21;  Length 357;
  Best Local Similarity   92.0%;  Pred. No. 0.00019;
  Matches   46;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 aattccctgttgacaattaatcatcgaactagttaactagtacgcagctt 51
          | | ||||||||||||||||||||||||||||||||||||||||  ||
Db    271 attcccctgttgacaattaatcatcgaactagttaactagtacgcaagtt 320
```

RESULT 12
AAA95073
ID AAA95073 standard; DNA; 357 BP.
XX
AC AAA95073;
XX
DT 18-JAN-2001 (first entry)
XX
DE trp promoter.
XX
KW Soybean; aminopeptidease; seasoning; R2219_2A; trp; promoter; ss.
XX
OS Unidentifed.
XX
FH Key Location/Qualifiers
FT promoter 1..357
FT /*tag= a
XX
PN EP1036843-A1.

XX
PD 20-SEP-2000.
XX
PF 15-MAR-2000; 2000EP-0105313.
XX
PR 15-MAR-1999; 99JP-0068255.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Ninomiya D, Miwa T, Asano M, Nakamura N, Nio N;
XX
DR WPI; 2000-595542/57.
XX
PT DNA encoding germinating soybean aminopeptidase and recombinant
PT production useful for producing highly hydrolyzed products -
XX
PS Example 2; Page 16; 25pp; English.
XX
CC The present invention relates to soybean aminopeptidase. The cDNA
CC encoding this protein was isolated by screening a soybean shoot cDNA
CC library using rice EST R2219_2A as a probe. The soybean aminopeptidase
CC cDNA may be used for the mass recombinant production of soybean
CC aminopeptidase, especially in Escherichia coli. The aminopeptidase is
CC useful for producing a highly hydrolyzed product from a highly acidic
CC protein. This may be used for seasoning. The present sequence is
CC the trp promoter. This was used in an aminopeptidase expression
CC plasmid.
XX
SQ Sequence 357 BP; 95 A; 90 C; 82 G; 90 T; 0 other;

Query Match 36.0%; Score 43.6; DB 21; Length 357;
Best Local Similarity 92.0%; Pred. No. 0.00019;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 aattccctgttgacaattaatcatcgaactagttaactagtacgcagctt 51
| | ||||||||||||||||||||||||||||||||||||||||||| ||
Db 271 attcccctgttgacaattaatcatcgaactagttaactagtacgcaagtt 320

RESULT 13
AAV81508
ID AAV81508 standard; DNA; 1519 BP.
XX
AC AAV81508;
XX
DT 01-APR-1999 (first entry)
XX
DE High expression transglutaminase gene present in pTRPMTG-02.
XX
KW Transglutaminase; microbial; gelled food; jelly; yogurt; cheese;
KW cosmetic; meat quality; microcapsule production; high thermal stability;
KW carrier; immobilised enzyme; ds.
XX
OS Synthetic.
OS Streptoverticillium sp.
XX
FH Key Location/Qualifiers
FT CDS 87..1085
FT /*tag= a
FT /product= transglutaminase
XX
PN EP889133-A2.
XX
PD 07-JAN-1999.
XX
PF 02-JUL-1998; 98EP-0112315.
XX
PR 04-JUL-1997; 97JP-0180010.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Miwa T, Nakamura N, Seguro K, Yokoyama K;
XX
DR WPI; 1999-062664/06.
DR P-PSDB; AAW67771.
XX
PT New microbial transglutaminase with N-terminal aspartic acid deleted
PT - allowing high level recombinant production without added
PT methionine in E. coli, useful in production of gelled foods,
PT cosmetics etc.
XX
PS Example 1; Page 18-23; 56pp; English.
XX
CC The present sequence represents the high expression transglutaminase
CC gene present in plasmid pTRPMTG-02. The gene is derived from
CC Streptoverticillium sp., and is codon altered, using oligonucleotides
CC AAV81521-60, for expression in Escherichia coli. The specification
CC describes a new microbial transglutaminase that has the N-terminal
CC aspartic acid of transglutaminase deleted. Eliminating the N-terminal
CC Asp from microbial transglutaminase allows efficient removal of the
CC terminal Met residue added when the protein is expressed in E. coli.
CC The E. coli methionine aminopeptidase acts well on Met-Ser but only
CC poorly on Met-Asp, so problems of antigenicity associated with
CC Met-terminated proteins are avoided. Recombinant transglutaminase is
CC used to produce gelled foods (jellies, yogurt and cheeses) or cosmetics,
CC to improve the quality of meat, in the production of materials for
CC microcapsules of high thermal stability and as a carrier for immobilised
CC enzymes.
XX
SQ Sequence 1519 BP; 355 A; 350 C; 387 G; 427 T; 0 other;

Query Match 35.7%; Score 43.2; DB 20; Length 1519;
Best Local Similarity 93.8%; Pred. No. 0.00035;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ttccctgttgacaattaatcatcgaactagttaactagtacgcagctt 51
| |||||||||||||||||||||||||||||||||||||||||| ||
Db 2 tcccctgttgacaattaatcatcgaactagttaactagtacgcaagtt 49

RESULT 14
AAA73025
ID AAA73025 standard; DNA; 1519 BP.
XX
AC AAA73025;
XX
DT 24-NOV-2000 (first entry)
XX
DE Transglutaminase nucleotide sequence SEQ ID NO:1.
XX
KW Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic;
KW cheese; ds.
XX
OS Unidentified.
XX
PN WO200040706-A1.
XX
PD 13-JUL-2000.
XX
PF 24-DEC-1999; 99WO-JP07250.
XX
PR 28-DEC-1998; 98JP-0373131.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Yokoyama K, Ono K, Ejima D;
XX
DR WPI; 2000-475826/41.
DR P-PSDB; AAB12809.
XX
PT Production of active transglutaminase from denatured enzyme by
PT two-stage refolding process for industrial production of active enzyme
PT for use in food production -
XX

```
PS   Disclosure; Page 48-50; 74pp; Japanese.
XX
CC   The present invention describes a method for producing active
CC   transglutaminase from denatured enzyme. The method comprises: (i) forming
CC   an intermediate structure of the enzyme having transglutaminase activity
CC   under acidic conditions in an aqueous medium; and (ii) forming a higher-
CC   level structure of the enzyme having transglutaminase activity under
CC   neutral conditions in an aqueous medium. The method can be used for
CC   industrial production of active transglutaminase from denatured material
CC   (such as recombinant transglutaminase) which can be used in the food
CC   industry for the production of gelled foods such as jellies, yoghurts
CC   and cheeses, and for the production of gelled cosmetics. The present
CC   sequence encodes a transglutaminase which is used in the exemplification
CC   from the present invention.
XX
SQ   Sequence 1519 BP; 355 A; 350 C; 387 G; 427 T; 0 other;


  Query Match             35.7%;  Score 43.2;  DB 21;  Length 1519;
  Best Local Similarity   93.8%;  Pred. No. 0.00035;
  Matches   45;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 ttcccctgttgacaattaatcatcgaactagttaactagtacgcagctt 51
          | ||||||||||||||||||||||||||||||||||||||||||||  ||
Db      2 tcccctgttgacaattaatcatcgaactagttaactagtacgcaagtt 49


RESULT  15
AAN50137
ID   AAN50137 standard; DNA; 63 BP.
XX
AC   AAN50137;
XX
DT   23-OCT-1991  (first entry)
XX
DE   Trp promoter.
XX
KW   Promoter; ss.
XX
FH   Key             Location/Qualifiers
FT   -35_signal      5..10
FT                   /*tag=  a
FT   -10_signal      28..33
FT                   /*tag=  b
FT   RBS             55..58
FT                   /*tag=  c
FT                   /label= Shine-Dalgarno
XX
PN   EP152830-A.
XX
PD   28-AUG-1985.
XX
PF   31-JAN-1985;   85EP-0100976.
XX
PR   02-FEB-1984;   84JP-0018133.
XX
PA   (GREC ) GREEN CROSS CORP.
XX
PI   Nakagawa Y,  Uno S,  Nagai M,  Arimura H;
XX
DR   WPI; 1985-211449/35.
XX
PT   Vector having promoter(s) between enzyme cleavage sites - for
PT   transforming Escherichia coli to give more efficient protein
PT   synthesis.
XX
PS   Claim 10; Page 26; 38pp; English.
XX
CC   The trp promoter is used in the construction of novel vectors
CC   which are used for more efficient protein synthesis in a
CC   transformed host.
XX
SQ   Sequence 63 BP; 22 A; 13 C; 11 G; 17 T; 0 other;


  Query Match             35.4%;  Score 42.8;  DB 6;  Length 63;
  Best Local Similarity   95.7%;  Pred. No. 0.00024;
  Matches   44;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      6 ccctgttgacaattaatcatcgaactagttaactagtacgcagctt 51
          ||||||||||||||||||||||||||||||||||||||||||||  ||
Db      1 ccctgttgacaattaatcatcgaactagttaactagtacgcaagtt 46


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Job time: 7699 sec
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